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3'UTR seed matches, but not overall identity, are associated with RNAi off-targets

A Birmingham, EM Anderson, A Reynolds, D Iisley- ... - Nature Methods, 2006 - nature.com

... There is a Corrigendum (June 2007) associated with this **Article**. ... that contain matches with any given siRNA **seed** region is very large in **comparison** to the ...

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BLAT-The BLAST-Like Alignment Tool - [*genome.org](#) (HTML)

WJ Kent - Genome Research, 2002 - Cold Spring Harbor Lab

... Looking at Table 4, to **compare** a translated mouse read ... and always uses a single perfect match as a **seed**. ... The publication costs of this **article** were defrayed in ...

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[PDF] ***Automated generation of heuristics for biological sequence comparison**

GS Slater, E Birney - BMC Bioinformatics, 2005 - biomedcentral.com

... is an Open Access **article** distributed under ... Heuristics for sequence **comparison** (such as BLAST [3 ... ap- plied to rectangular regions surrounding **alignment seeds**. ...

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[HTML] ***Protein homology detection by HMM-HMM comparison**

J Soding - Bioinformatics, 2005 - Oxford Univ Press

... **Articles** by Soding, J ... HHsearch 0 uses simple profile-profile **comparison** by setting all gap opening ... **alignment** that have a residue in the **seed** sequence instead ...

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[HTML] ***Fast and sensitive multiple alignment of large genomic sequences**

M Brudno, M Chapman, B Gottgens, S Batzoglu, B ... - BMC Bioinformatics, 2003 - biomedcentral.com

... is preserved along with the **article's** original URL. ... data are presently available to **compare** the performance ... The **seeds** are located **using** a simplified version of ...

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AVID: A Global Alignment Program - [*stanford.edu](#) (PDF)

N Bray, I Dubchak, L Pachter - Genome Research, 2003 - Cold Spring Harbor Lab

... running AVID and displaying alignments **using** VISTA is ... **Article** published online before print in December 2002. ... for large-scale genome **alignment** and **comparison**. ...

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A comparison of position-specific score matrices based on sequence and structure alignments - [*highwire.org](#) (HTML)

AR Panchenko, SH Bryant - Protein Science, 2002 - protsci.highwire.org

... **Article** and publication are at <http://www.proteinscience.org> ... used to construct the **seed alignment** upon which ... We **compare** PSSMs based on alignments constructed by ...

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CE-MC: a multiple protein structure alignment server. - [*nih.gov](#) (HTML)

C Guda, S Lu, ED Scheeff, PE Bourne, IN Shindyalov - Nucleic Acids Research, 2004 - pt.wkhealth.com

... correct citation details given; if an **article** is subsequently ... optimized by all-to-all **comparison** of protein ... Initial **seed** alignments are assembled from pairwise ...

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Protein sequence similarity searches using patterns as seeds - [*fb-sargau.ch](#) (PDF)

Z Zhang, AA Schaffer, W Miller, TL Madden, DJ ... - Nucleic Acids Research - Oxford Univ Press

... number of distinct pattern pairs that may **seed** a PHI ... particularly valuable, and a DNA-DNA **comparison** version should ... This **article** has been cited by other **articles** ...

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[HTML] • [ProSup: a refined tool for protein structure alignment](#)

P Lackner, WA Koppensteiner, MJ Sippl, FS ... - Protein Engineering Design and Selection, 2000 - Oxford Univ Press

... Alert me when: new **articles** cite this **article**. ... based on the **alignment** of distance matrices, (3) **compare** the ProSup ... In step (3) a **seed alignment** is refined by a ...

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